

**IN THE SPECIFICATION:**

Please replace Paragraph No. 00055 with the following paragraph:

-- The present invention provides purified and isolated polynucleotides (*e.g.*, DNA sequences and RNA transcripts, both sense and complementary antisense strands, both single- and double-stranded, including splice variants thereof) that encode unknown G protein-coupled receptors heretofore termed novel GPCRs, or nGPCRs. The gene described herein is referred to as nGPCR-2644. Table 1 below identifies the SEQ ID NO: of the gene sequence, the SEQ ID NO: of the polypeptide encoded thereby, and the U.S. Provisional Application in which the gene sequence has been disclosed.

**Table 1**

nGPCR	Nucleotide Sequence (SEQ ID NO:)	Amino acid Sequence (SEQ ID NO:)	Originally filed in:
2644	1	2	A

**Legend**

A= Ser. No. 60/199,558

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Please replace Paragraph No. 00119 with the following paragraph:

-- Variant polypeptides include those wherein conservative substitutions have been introduced by modification of polynucleotides encoding polypeptides of the invention. Amino acids can be classified according to physical properties and contribution to secondary and tertiary protein structure. A conservative substitution is recognized in the art as a substitution of one amino acid for another amino acid that has similar properties. Exemplary conservative substitutions are set out in Table 2 (from WO 97/09433, page 10, published March 13, 1997 (PCT/GB96/02197, filed 9/6/96), immediately below.

**Table 2**

**Conservative Substitutions I**

**SIDE CHAIN**

<u>CHARACTERISTIC</u>	<u>AMINO ACID</u>
Aliphatic	
Non-polar	G A P I L V
Polar - uncharged	C S T M N Q
Polar - charged	D E K R
Aromatic	H F W Y
Other	N Q D E --

Please replace Paragraph No. 00120 with the following paragraph:

-- Alternatively, conservative amino acids can be grouped as described in Lehninger, (Biochemistry, Second Edition; Worth Publishers, Inc. NY, NY (1975), pp.71-77) as set out in Table 3, below.

**Table 3**  
**Conservative Substitutions II**

<u>SIDE CHAIN</u>	<u>CHARACTERISTIC</u>	<u>AMINO ACID</u>
Non-polar (hydrophobic)		
A. Aliphatic:		A L I V P
B. Aromatic:		F W
C. Sulfur-containing:		M
D. Borderline:		G
Uncharged-polar		
A. Hydroxyl:		S T Y
B. Amides:		N Q
C. Sulfhydryl:		C
D. Borderline:		G
Positively Charged (Basic):		K R H
Negatively Charged (Acidic):		D E --

Please replace Paragraph No. 00236 with the following paragraph:

-- The following Table 5 contains the sequences of the polynucleotides and polypeptides of the invention. The transmembrane domains within the polypeptide sequence are identified by underlining, and start and stop sites are identified by bold text.

Table 5

The following DNA sequence nGPCR-2644 <SEQ ID NO. 1> was identified in *H. sapiens*:

[illegible]

The following amino acid sequence <SEQ ID NO. 2> is a predicted amino acid sequence derived from the DNA sequence of SEQ ID NO. 1:

<SEQ ID NO. 2>

MTTNTNSTRESNJGHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKEQ  
LLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLEFWPLNSHFCTALVSLTHLFAFASVNTI  
VVVSVPRYLSCIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAPERNALCS  
MIWACFSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVPVKDVEN  
EDEEAEKKKEEFQDEMNIPESLPPSRNRNSNPLPRCYQCKAAKVIFIIIFSYVLSLGPY  
CELAVLAVWVDVETQVPQWVITIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLNKKFFKE  
KPIKEDSHFTLPGTGGTEGKIVPSYDSATFI

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